



#8

1

EXPRESS MAIL NO. EL755728058US

## SEQUENCE LISTING

<110> White, Aaron P.  
Doran, James L.  
Collinson, S. Karen  
Kay, William W.

<120> BACTERIAL FIMBRIAL SYSTEM FOR  
PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

<130> 920043.406

<140> US 09/543,407

<141> 2000-04-05

<160> 59

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 456

<212> DNA

<213> Salmonella enteritidis

<400> 1

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ggcgctcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc	120
ccggactcaa cggtgagcat ttatcagtac gggtccgcta acgctgcgct tgctctgcaa	180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat	240
gtaggccagg gtgcgggataa tagtactatt gaactgactc agaatggttt cagaaataat	300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt	360
aataacgccc cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt	420
ggttttggca acaacgccac ggctaaccag tatta	456

<210> 2

<211> 456

<212> DNA

<213> Salmonella enteritidis

<400> 2

atgaaaaaca aattgttatt tatgatgttg acaatactgg gtgcgcctgg gattgcaacc	60
gcgcacaaatt atgatctggc tcgttcagaa tataattttg cggtaaatga attaagcaag	120
tcttcattta atcaggcggc cattatttgt caagtcggca cgataatag tgccagagta	180
cgccaggaag gatcaaaact attgtccgtt atttcacaag aaggaggaaa taatcgggcy	240
aaagtcgacc aggcaggga ttataacttt gcgtatattg agcaaacggg caatgccaac	300
gatgccagta tatcgaaaag cgcttacggg aatagtgcag ctattatcca gaaaggttct	360
ggaaataagg ccaatattac ccagtacggg acgcagaaa cagcagttgt agtgcagaaa	420
cagtcgcata tggctattcg cgtcacccaa cgctaa	456

<210> 3

<211> 456  
 <212> DNA  
 <213> E. Coli

<400> 3  
 atgaaaacttt taaaagtaga agcaattgca gcaatcgat tctccggtag cgctctggca 60  
 ggtgttggtc ctacgtacgg cggcggcggg aaccacgggt gtggcggtaa taatagcggc 120  
 ccaaattctg agctgaacat ttaccagtac ggtggcggtg actctgcact tgctctgcaa 180  
 actgatgcc gtaactctga cttgactatt acccagcatg gcggcggtaa tggcgcagat 240  
 gttggtcagg gctcagatga cagctcaatc gatctgaccc aacgtggctt cggtaacagc 300  
 gctactcttg atcagtgga cggcaaaaat tctgaaatga cgggttaaaca gtccgggtgt 360  
 ggcaacgggtg ctgcagttga ccagactgca tctaactcct ccgtcaacgt gactcaggtt 420  
 ggctttggta acaacgcgac cgctcatcag tactaa 456

<210> 4  
 <211> 456  
 <212> DNA  
 <213> E. Coli

<400> 4  
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 gcagcagggt atgatttagc taattcagaa tataacttcg cggtaaatga attgagtaag 120  
 tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtta 180  
 cggcagggag gctcaaaact tttggcgggt gttgcgcaag aaggtagtag caaccgggca 240  
 aagattgacc agacaggaga ttataacctt gcataatatt atcaggcggg cagtgcacac 300  
 gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct 360  
 ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga 420  
 cagtcgcaaa tggctatttc cgtgacacaa cggttaa 456

<210> 5  
 <211> 151  
 <212> PRT  
 <213> Salmonella enteritidis

<400> 5  
 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly  
 1 5 10 15  
 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His  
 20 25 30  
 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr  
 35 40 45  
 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg  
 50 55 60  
 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp  
 65 70 75 80  
 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly  
 85 90 95  
 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp  
 100 105 110  
 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln  
 115 120 125  
 Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn  
 130 135 140  
 Asn Ala Thr Ala Asn Gln Tyr

145

150

&lt;210&gt; 6

&lt;211&gt; 151

&lt;212&gt; PRT

<213> *Salmonella enteritidis*

&lt;400&gt; 6

```

Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
 1           5           10           15
Gly Ile Ala Thr Ala Thr Asn Tyr Asp Leu Ala Arg Ser Glu Tyr Asn
          20          25          30
Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
          35          40          45
Ile Gly Gln Val Gly Thr Asp Asn Ser Ala Arg Val Arg Gln Glu Gly
          50          55          60
Ser Lys Leu Leu Ser Val Ile Ser Gln Glu Gly Gly Asn Asn Arg Ala
65          70          75          80
Lys Val Asp Gln Ala Gly Asn Tyr Asn Phe Ala Tyr Ile Glu Gln Thr
          85          90          95
Gly Asn Ala Asn Asp Ala Ser Ile Ser Gln Ser Ala Tyr Gly Asn Ser
          100         105         110
Ala Ala Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
          115         120         125
Tyr Gly Thr Gln Lys Thr Ala Val Val Val Gln Lys Gln Ser His Met
          130         135         140
Ala Ile Arg Val Thr Gln Arg
145          150

```

&lt;210&gt; 7

&lt;211&gt; 151

&lt;212&gt; PRT

<213> *Escherichia coli*

&lt;400&gt; 7

```

Met Lys Leu Leu Lys Val Ala Ala Ile Ala Ala Ile Val Phe Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Tyr Gly Gly Gly Gly Asn His
          20          25          30
Gly Gly Gly Gly Asn Asn Ser Gly Pro Asn Ser Glu Leu Asn Ile Tyr
          35          40          45
Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala Leu Gln Thr Asp Ala Arg
          50          55          60
Asn Ser Asp Leu Thr Ile Thr Gln His Gly Gly Gly Asn Gly Ala Asp
65          70          75          80
Val Gly Gln Gly Ser Asp Asp Ser Ser Ile Asp Leu Thr Gln Arg Gly
          85          90          95
Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp Asn Gly Lys Asn Ser Glu
          100         105         110
Met Thr Val Lys Gln Phe Gly Gly Asn Gly Ala Ala Val Asp Gln
          115         120         125
Thr Ala Ser Asn Ser Ser Val Asn Val Thr Gln Val Gly Phe Gly Asn
          130         135         140
Asn Ala Thr Ala His Gln Tyr

```

145                      150

<210> 8  
 <211> 151  
 <212> PRT  
 <213> Escherichia coli

<400> 8  
 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro  
   1                  5                  10                  15  
 Gly Ile Ala Ala Ala Gly Tyr Asp Leu Ala Asn Ser Glu Tyr Asn  
           20                  25                  30  
 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile  
       35                  40                  45  
 Ile Gly Gln Ala Gly Thr Asn Asn Ser Ala Gln Leu Arg Gln Gly Gly  
   50                  55                  60  
 Ser Lys Leu Leu Ala Val Val Ala Gln Glu Gly Ser Ser Asn Arg Ala  
 65                  70                  75                  80  
 Lys Ile Asp Gln Thr Gly Asp Tyr Asn Leu Ala Tyr Ile Asp Gln Ala  
                   85                  90                  95  
 Gly Ser Ala Asn Asp Ala Ser Ile Ser Gln Gly Ala Tyr Gly Asn Thr  
           100                  105                  110  
 Ala Met Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln  
           115                  120                  125  
 Tyr Gly Thr Gln Lys Thr Ala Ile Val Val Gln Arg Gln Ser Gln Met  
   130                  135                  140  
 Ala Ile Arg Val Thr Gln Arg  
 145                  150

<210> 9  
 <211> 48  
 <212> DNA  
 <213> Leishmania major

<400> 9  
 tatgatcagc tgggtaccgc tggtgttacc catgaaatgg cacatgca

48

<210> 10  
 <211> 16  
 <212> PRT  
 <213> Leishmania major

<400> 10  
 Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala  
   1                  5                  10                  15

<210> 11  
 <211> 456  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Recombinant Salmonella enteritidis 3b afgA  
       sequence containing the replacement fragment

encoding PT3 from GP63 of *Leishmania major*.

```
<400> 11
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct    60
ggcgtcggtt cacaatgggg cggcgggcgt aatcataacg gcggcgggcaa tagttccggc    120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa    180
agcgatgccc gtaaattctga aacgaccatt acccagagcg gttatggtaa cggcgccgat    240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat    300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt    360
aataacgccg cgctgggttaa ttatgatcag ctggttaccc gtgttggttac ccatgaaatg    420
gcacatgcaa acaacgccac ggctaaccag tattaa                                456
```

```
<210> 12
<211> 151
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.
```

```
<400> 12
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1             5             10             15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20             25             30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35             40             45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50             55             60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65             70             75             80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85             90             95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100             105             110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Tyr
      115             120             125
Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn
      130             135             140
Asn Ala Thr Ala Asn Gln Tyr
145             150
```

```
<210> 13
<211> 456
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.
```

```

<400> 13
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttcgcta acgtgcgtt tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atatgatcag      360
ctggttaccc gtgttggttac ccatgaaatg gcacatgcaa gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

```

<210> 14
<211> 151
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.

```

```

<400> 14
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20          25          30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
          35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
          50          55          60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65          70          75          80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100         105         110
Ile Thr Val Gly Gln Tyr Asp Gln Leu Val Thr Arg Val Val Thr His
          115         120         125
Glu Met Ala His Ala Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
          130         135         140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

```

<210> 15
<211> 456
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.

```

```

<400> 15
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60

```

```

ggcgtctatg atcagctggt taccgtggt gttacccatg aaatggcaca tgcattccggc 120
ccggactcaa cggtgagcat ttatcagtac gggtccgcta acgctgcgct tgctctgcaa 180
agcgatgccc gtaaattctga aacgaccatt acccagagcg gttatggtaa cggcgccgat 240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatgggtt cagaaataat 300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420
ggttttggca acaacgccac ggctaaccag tattaa 456

```

<210> 16  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Recombinant *Salmonella enteritidis* 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 16
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1             5             10             15
Ser Ala Leu Ala Gly Val Tyr Asp Gln Leu Val Thr Arg Val Val Thr
      20             25             30
His Glu Met Ala His Ala Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35             40             45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50             55             60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65             70             75             80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85             90             95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100            105            110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115            120            125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130            135            140
Asn Ala Thr Ala Asn Gln Tyr
145            150

```

<210> 17  
 <211> 456  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Recombinant *Salmonella enteritidis* 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 17
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60
ggcgtcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc 120
ccggactatg atcagctggt taccgtggt gttacccatg aaatggcaca tgcaactgcaa 180

```

```

agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccc cgctgggtaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

<210> 18  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Recombinant Salmonella enteritidis 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of Leishmania major.

```

<400> 18
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1             5             10             15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20             25             30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Tyr Asp Gln Leu Val Thr
      35             40             45
Arg Val Val Thr His Glu Met Ala His Ala Leu Gln Ser Asp Ala Arg
      50             55             60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
      65             70             75             80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85             90             95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100            105            110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115            120            125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130            135            140
Asn Ala Thr Ala Asn Gln Tyr
145                        150

```

<210> 19  
 <211> 456  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Recombinant Salmonella enteritidis 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of Leishmania major.

```

<400> 19
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgctcgtt cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaatatga tcagctgggt acccggtgtt ttacccatga aatggcacat      240
gcaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300

```



```

gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420
ggttttggca acaacgccac ggctaaccag tattaa 456

```

<210> 20  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Recombinant Salmonella enteritidis 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of Leishmania major.

```

<400> 20
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
        35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
        50           55           60
Lys Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His
        65           70           75           80
Ala Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
          115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
          130          135          140
Asn Ala Thr Ala Asn Gln Tyr
          145          150

```

<210> 21  
 <211> 456  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Recombinant Salmonella enteritidis 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of Leishmania major.

```

<400> 21
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60
ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc 120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa 180
agcgatgccc gtaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgat 240
gtaggccagg gtgcgggataa ttatgatcag ctgggttacc gtgttggtac ccatgaaatg 300
gcacatgcag accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420

```

ggttttggca acaacgccac ggctaaccag tattaa

456

<210> 22

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 22

Met	Lys	Leu	Leu	Lys	Val	Ala	Ala	Phe	Ala	Ala	Ile	Val	Val	Ser	Gly
1				5				10						15	
Ser	Ala	Leu	Ala	Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Gly	Asn	His
			20					25					30		
Asn	Gly	Gly	Gly	Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr
			35				40					45			
Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Ala	Leu	Ala	Leu	Gln	Ser	Asp	Ala	Arg
			50			55				60					
Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly	Ala	Asp
65					70				75					80	
Val	Gly	Gln	Gly	Ala	Asp	Asn	Tyr	Asp	Gln	Leu	Val	Thr	Arg	Val	Val
				85				90					95		
Thr	His	Glu	Met	Ala	His	Ala	Asp	Gln	Trp	Asn	Ala	Lys	Asn	Ser	Asp
			100				105					110			
Ile	Thr	Val	Gly	Gln	Tyr	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Gln
		115				120					125				
Thr	Ala	Ser	Asp	Ser	Ser	Val	Met	Val	Arg	Gln	Val	Gly	Phe	Gly	Asn
	130					135					140				
Asn	Ala	Thr	Ala	Asn	Gln	Tyr									
145					150										

<210> 23

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 23

atgaaacttt	taaaagtggc	agcattcgca	gcaatcgtag	tttctggcag	tgctctggct	60
ggcgctcggtc	cacaatgggg	cggcgggcgg	aatcataacg	gcggcgggcaa	tagttccggc	120
ccggactcaa	cgttgagcat	ttatcagtac	ggttccgcta	acgctgcgct	tgctctgcaa	180
agcgatgccc	gtaaactctga	aacgaccatt	accagagcg	ggttatggtaa	cggcgccgat	240
gtaggccagg	gtgcggataa	tagtactatt	gaactgactc	agaatggttt	cagaaataat	300
gccaccatcg	accagtggaa	cgctaaaaac	tatgatcagc	tggttaccgc	tggtgttacc	360
catgaaatgg	cacatgcaaa	tcagaccgca	tctgattcca	gcgtaatggg	gcgtcaggtt	420
ggttttggca	acaacgccac	ggctaaccag	tattaa			456

<210> 24  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of *Leishmania major*.

<400> 24

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Tyr Asp
      100          105          110
Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn Gln
      115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145           150

```

<210> 25  
 <211> 456  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of *Leishmania major*.

<400> 25

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgctcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct ttatgatcag      180
ctggttaccc gtgttggttac ccatgaaatg gcacatgcag gttatggttaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggg gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa      456

```

<210> 26  
 <211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 26

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Tyr Asp Gln Leu Val Thr Arg
      50           55           60
Val Val Thr His Glu Met Ala His Ala Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145           150

```

<210> 27

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 27

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcggtc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
tatgatcagc tggttacccg tgttgttacc catgaaatgg cacatgcatt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa      456

```

<210> 28

<211> 151

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

&lt;400&gt; 28

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
          35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
          50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala
          85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
          115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
          130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145           150

```

&lt;210&gt; 29

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

&lt;400&gt; 29

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcggtc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcgggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccacctatg atcagctggg taccgcgtgt gttacccatg aaatggcaca tgcaggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggg gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

&lt;210&gt; 30

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 30

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
 50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85           90           95
Phe Arg Asn Asn Ala Thr Tyr Asp Gln Leu Val Thr Arg Val Val Thr
          100           105           110
His Glu Met Ala His Ala Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115           120           125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130           135           140
Asn Ala Thr Ala Asn Gln Tyr
145           150

```

<210> 31

<211> 131

<212> PRT

<213> *Salmonella enteritidis*

<400> 31

```

Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His Asn Gly Gly Gly
 1           5           10           15
Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser
      20           25           30
Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr
      35           40           45
Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly
 50           55           60
Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn
65           70           75           80
Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp Ile Thr Val Gly
      85           90           95
Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln Thr Ala Ser Asp
      100           105           110
Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn Asn Ala Thr Ala
      115           120           125
Asn Gln Tyr
130

```

<210> 32

<211> 70

<212> PRT

<213> *Salmonella enteritidis*

<400> 32

```

Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly
 1           5           10           15
Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln
          20           25           30
Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Lys Asn Asp
          35           40           45
Ile Val Gly Tyr Gly Asn Ala Leu Asn Thr Ser Asp Ser Val Met Val
          50           55           60
Arg Val Gly Ala Asn Tyr
65           70

```

<210> 33

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence of the five internal repeats of AgfA.

<221> VARIANT

<222> (1)...(23)

<223> Xaa = Any Amino Acid

<400> 33

```

Ser Xaa Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Xaa Asn Xaa Ala Xaa Xaa
 1           5           10           15
Xaa Gln Xaa Xaa Ala Xaa Xaa
          20

```

<210> 34

<211> 109

<212> PRT

<213> *Salmonella enteritidis*

<400> 34

```

Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala
 1           5           10           15
Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly
          20           25           30
Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile
          35           40           45
Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp
          50           55           60
Asn Ala Lys Asn Ser Asp Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn
65           70           75           80
Ala Ala Leu Val Asn Gln Thr Ala Ser Asp Ser Ser Val Met Val Arg
          85           90           95
Gln Val Gly Phe Gly Asn Asn Ala Thr Ala Asn Gln Tyr
          100          105

```

<210> 35  
 <211> 109  
 <212> PRT  
 <213> *Escherichia coli*

<400> 35  
 Ser Glu Leu Asn Ile Tyr Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala  
 1 5 10 15  
 Leu Gln Thr Asp Ala Arg Asn Ser Asp Leu Thr Ile Thr Gln His Gly  
 20 25 30  
 Gly Gly Asn Gly Ala Asp Val Gly Gln Gly Ser Asp Asp Ser Ser Ile  
 35 40 45  
 Asp Leu Thr Gln Arg Gly Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp  
 50 55 60  
 Asn Gly Lys Asn Ser Glu Met Thr Val Lys Gln Phe Gly Gly Gly Asn  
 65 70 75 80  
 Gly Ala Ala Val Asp Gln Thr Ala Ser Asn Ser Ser Val Asn Val Thr  
 85 90 95  
 Gln Val Gly Phe Gly Asn Asn Ala Thr Ala His Gln Tyr  
 100 105

<210> 36  
 <211> 56  
 <212> PRT  
 <213> *Serratia marcescens*

<400> 36  
 Ile Glu Asn Ala Ile Gly Gly Ser Gly Asn Asp Val Ile Val Gly Asn  
 1 5 10 15  
 Ala Ala Asn Asn Val Leu Lys Gly Gly Ala Gly Asn Asp Val Leu Phe  
 20 25 30  
 Gly Gly Gly Gly Ala Asp Glu Leu Trp Gly Gly Ala Gly Lys Asp Ile  
 35 40 45  
 Phe Val Phe Ser Ala Ala Ser Asp  
 50 55

<210> 37  
 <211> 68  
 <212> PRT  
 <213> *Salmonella enteritidis*

<400> 37  
 Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala  
 1 5 10 15  
 Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly  
 20 25 30  
 Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile  
 35 40 45  
 Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp  
 50 55 60  
 Asn Ala Lys Asn  
 65

<210> 38



<211> 47  
 <212> PRT  
 <213> bovine

<400> 38  
 Val Ile Ile Ser Lys Lys Gly Asp Ile Ile Thr Ile Arg Thr Glu Ser  
 1 5 10 15  
 Pro Phe Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly Gln Glu Phe Glu  
 20 25 30  
 Glu Thr Thr Ala Asp Asn Arg Lys Thr Lys Ser Thr Val Thr Leu  
 35 40 45

<210> 39  
 <211> 48  
 <212> PRT  
 <213> Salmonella enteritidis

<400> 39  
 Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln  
 1 5 10 15  
 Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly  
 20 25 30  
 Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu  
 35 40 45

<210> 40  
 <211> 19  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 40  
 Phe Ala Leu Lys Val Glu Pro Ser Gln Phe Gly Arg Asp Asp Thr Ala  
 1 5 10 15  
 Leu Asn Gly

<210> 41  
 <211> 19  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 41  
 Phe Ser Leu Arg Ser Glu Lys Ser Gln Gly Gly Gly Asp Asp Thr Ala  
 1 5 10 15  
 Ala Asn Asn

<210> 42  
 <211> 19  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 42  
 Leu Gln Thr Lys Val Glu Ser Pro Gln Gly Leu Arg Asp Asp Thr Ala  
 1 5 10 15  
 Leu Asn Asn

<210> 43  
 <211> 16  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 43  
 Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln  
 1 5 10 15

<210> 44  
 <211> 16  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 44  
 Ile Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln  
 1 5 10 15

<210> 45  
 <211> 16  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Beta-prism motif of the vitelline membrane outer  
 layer protein I (VMO-I)

<400> 45  
 Val Met Val Arg Gln Val Gly Phe Gly Asn Asn Ala Thr Ala Asn Gln  
 1 5 10 15

<210> 46  
 <211> 143  
 <212> PRT  
 <213> *Salmonella enteritidis*

<400> 46  
 Ala Gly Phe Val Gly Asn Lys Ala Val Val Gln Ala Ala Val Thr Ile  
 1 5 10 15  
 Ala Ala Gln Asn Thr Thr Ser Ala Asn Trp Ser Gln Asp Pro Gly Phe  
 20 25 30  
 Thr Gly Pro Ala Val Ala Ala Gly Gln Lys Val Gly Thr Leu Ser Ile  
 35 40 45  
 Thr Ala Thr Gly Pro His Asn Ser Val Ser Ile Ala Gly Lys Gly Ala  
 50 55 60  
 Ser Val Ser Gly Gly Val Ala Thr Val Pro Phe Val Asp Gly Gln Gly  
 65 70 75 80  
 Gln Pro Val Phe Arg Gly Arg Ile Gln Gly Ala Asn Ile Asn Asp Gln  
 85 90 95  
 Ala Asn Thr Gly Ile Asp Gly Leu Ala Gly Trp Arg Val Ala Ser Ser  
 100 105 110  
 Gln Glu Thr Leu Asn Val Pro Val Thr Thr Phe Gly Lys Ser Thr Leu  
 115 120 125  
 Pro Ala Gly Phe Thr Ala Thr Phe Tyr Val Gln Gln Tyr Gln Asn  
 130 135 140

<210> 47  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 47  
 ttggaattct tcttaaattt ttaaaatggc gttgagtat

39

<210> 48  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 48  
 agcatgagcc atttcatgtg taacaacacg tgtaacgagc tgatcatatg caatagtaac  
 cgctgcctga accactgc

60  
 78

<210> 49  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> PCR primer

<400> 49

tatgatcagc tcgttacacg tgttggtaca catgaaatgg ctcatgctgg gcctgctgtt 60  
gctgctggtc agaaagtt 78

<210> 50

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 50

attaagctta tacataatcc ctctttaagt ttttgcattg 39

<210> 51

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

gcagaattca gcagttgtag tgcagaaaca gtcgcatat 39

<210> 52

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

tgcattgtgcc atttcatggg taacaacacg ggtaaccagc tgatcatagt ttttagcgtt 60  
ccactggtcg atggtggc 78

<210> 53

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 53

tatgatcagc tggttaccgc tgttggtacc catgaaatgg cacatgcaaa tcagaccgca 60  
tctgattcca gcgtaattg 78

<210> 54

<211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 54  
 agacgcaagc ttcgtttaat gtgacctgag ggatcaccg 39  
  
 <210> 55  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 55  
 gggatgttgt gtaaagataa aaaaatagtg 30  
  
 <210> 56  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 56  
 tgcccaatct taggcataa tatttttgtg 30  
  
 <210> 57  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 57  
 aggaaggatc aaaactattg tccgttatTTT cac 33  
  
 <210> 58  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR primer  
  
 <400> 58  
 tatatttaca ctaagacgag acaactcaat cgg 33

<210> 59  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
<222> (1)...(18)  
<223> Xaa = Any Amino Acid

<400> 59  
Ser Xaa Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Xaa Asn Xaa Ala Xaa Xaa  
1 5 10 15  
Xaa Gln